

REPLACEMENT SHEET

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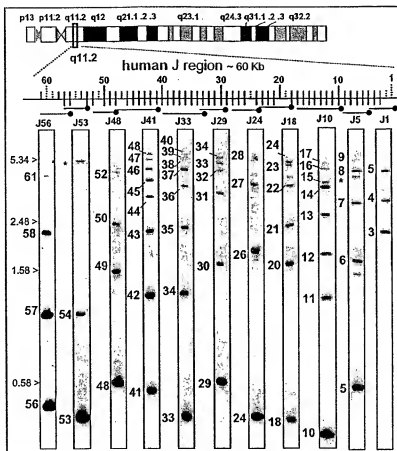


FIGURE 1

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REPLACEMENT SHEET

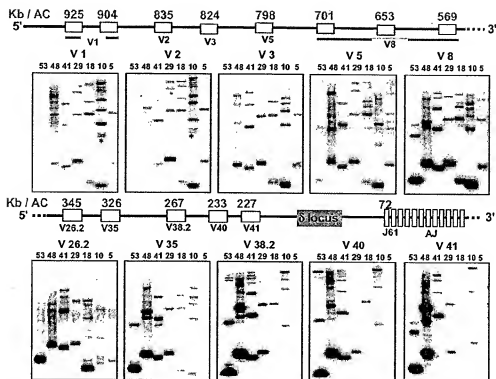


FIGURE 2

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REPLACEMENT SHEET

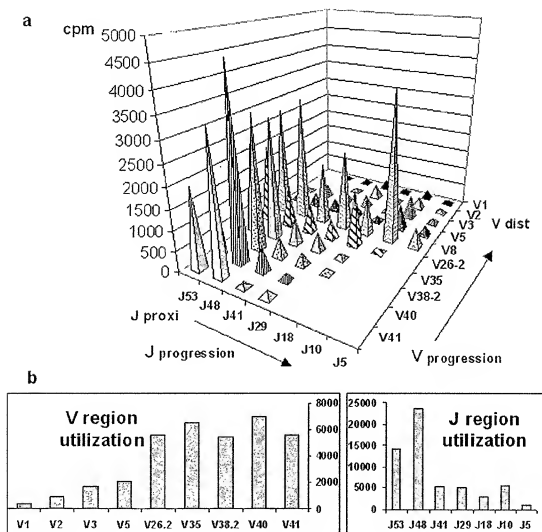


FIGURE 3

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REPLACEMENT SHEET

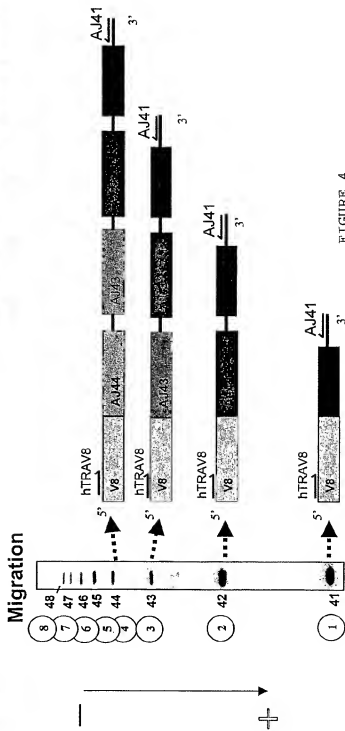
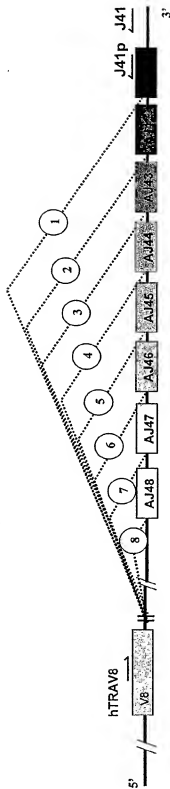


FIGURE 4

REPLACEMENT SHEET

hv gene	Heptamer	SEQ ID NO	%	Spacer	SEQ ID NO	%	Nonamer	SEQ ID NO	%	RSS score	Dist/Ca (Kb)	Signal dity	J tropism
hV1-1	CACAGTC	76	100	ACTAATGAGCCCTTAACTGTG	77	56	CAAAATTC	78	56	72	925	1604	J10
hV1-2	CACAGTC	79	86	ACTAATGAGCCCTTAACTGTCA	80	63	CAAAATTC	78	56	69	904	1604	J10
hV2	CACAGTC	81	86	GCAGGAGAGCCCTTAACTGTCA	82	56	CAAAATTC	78	56	75	835	1637	J10
hV3	CACAGTC	84	86	ATAGGCTCTGAGGAGAGCTGA	85	56	CAAAATTC	78	56	80	824	1940	J10
hV5	CACAGTC	87	86	ATAGGCTCTGAGGAGAGCTGA	88	94	CAAAATTC	78	56	93	798	2408	J10
hV8-2	CACAGTC	76	100	CTGTGAGCTGAGGAGAGCTGAA	90	50	CAAAATTC	78	56	63	701	15830	All J
hV8-4	CACAGTC	76	100	CTGTGAGCTGAGGAGAGCTGAA	90	50	CAAAATTC	78	56	63	653	15830	All J
hV8-6	CACAGTC	76	100	CTGTGAGCTGAGGAGAGCTGAA	90	50	CAAAATTC	78	56	65	589	15830	area
hV28-2	CACAGTC	76	100	GGACAGCTGAGGAGAGCTGAA	93	56	CAAAATTC	78	56	64	345	5638	J48
hV35	CACAGTC	76	100	CTCCGAGAACTGAGAGCTGTT	97	94	CAAAATTC	78	56	80	326	6520	J48
hV38-2	CACAGTC	76	100	AGCAGAGCACTGAGAGCTGTT	99	31	CAAAATTC	78	56	78	287	11008	J48
hV40	CACAGTC	101	86	ATAGGCTCTGAGGAGAGCTGA	102	44	CAAAATTC	78	56	60	233	6930	J48
hV41	CACAGTC	76	100	CTCCGAGAACTGAGAGCTGTT	104	94	CAAAATTC	78	56	90	227	5630	J48
Consensus	CACAGTC	76		CTCCGAGAACTGAGAGCTGTT	106		CAAAATTC	78	56	%			

FIGURE 5

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REPLACEMENT SHEET

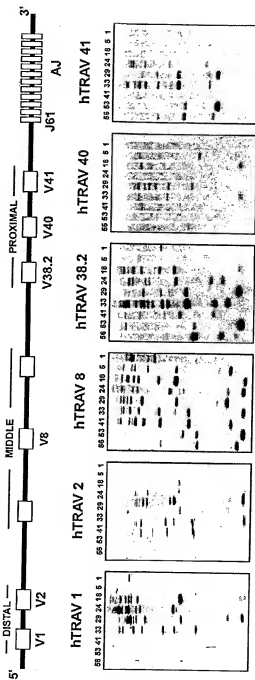


FIGURE 6

REPLACEMENT SHEET

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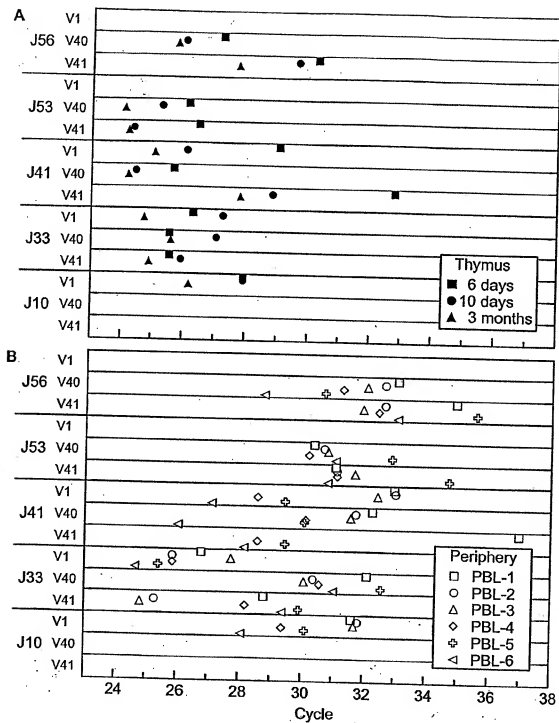


FIGURE 7

REPLACEMENT SHEET

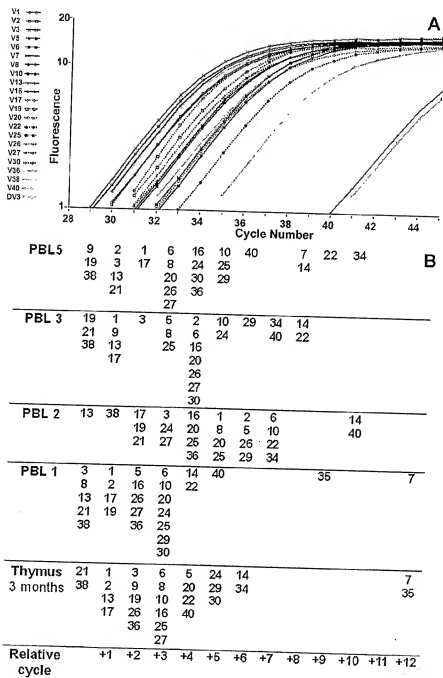


FIGURE 8